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GENOME ANNOUNCEMENT

Complete Genome Sequence of "*Candidatus* Portiera aleyrodidarum" BT-QVLC, an Obligate Symbiont That Supplies Amino Acids and Carotenoids to *Bemisia tabaci*

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The genome of "*Candidatus* Portiera aleyrodidarum," the primary endosymbiont of the whitefly *Bemisia tabaci* (Mediterranean species), is reported. It presents a reduced genome (357 kb) encoding the capability to synthetize, or participate in the synthesis of, several amino acids and carotenoids, being the first insect endosymbiont capable of supplying carotenoids.

Whiteflies are small sap-sucking insects belonging to the family Aleyrodidae (2). *Bemisia tabaci*, which is able to feed on many plant species, being one of the worst agricultural pests, has been described as a species complex composed of 24 indistinguishable species (formerly called biotypes) (3). The most important biotypes (based on economic losses) are B (or Middle East-Asia Minor 1 species), which is the most widespread, and Q (or Mediterranean species), which shows more resistance to insecticides (9).

B. tabaci harbors a primary (obligate) endosymbiont, "*Candidatus* Portiera aleyrodidarum," which is located in specialized cells called bacteriocytes (1), and also may contain different secondary (facultative) symbionts (7).

We report here the complete genome of the primary symbiont "*Ca.* Portiera aleyrodidarum" BT-QVLC from *B. tabaci* (Mediterranean species) strain QHC-VLC, which also harbors "*Candidatus* Hamiltonella defensa" (13) and "*Candidatus* Cardinium hertigii" (20).

Enriched bacterial samples were obtained by following a modified Harrison protocol (8) and used for sequencing single-end and 3-kb pair-end libraries using 454 GS-FLX Titanium and a 5-kb mate-pair using HiSeq2000. Filtered reads were used for MIRA *de novo* hybrid assembly, and the software program Gap4 was used for editing and closing the genome (41× combined coverage). The software program Prodigal and the BASYS and RAST servers were used for the initial gene calling, followed by hand curation.

"*Ca.* Portiera aleyrodidarum" has a small chromosome (357,472 bp) with 26.1% G+C content and 68% coding density, values derived from a strong genome reduction process (5, 12, 14), being in the frontier between reduced and extremely reduced symbiotic genomes (10, 11, 16). The genome contains 246 coding genes, 8 pseudogenes, and 38 noncoding RNA genes (33 tRNAs, 3 rRNAs, *rnpB*, and tmRNA). It includes an almost complete information transfer gene repertoire (4) but lacks the genes encoding the aminoacyl-tRNA synthetases for arginine, methionine, threonine, and tryptophan. "*Ca.* Portiera aleyrodidarum" is able to synthesize the essential amino acids threonine and tryptophan and the nonessential serine and lacks the last gene of the phenylalanine, valine, leucine, and isoleucine pathways. The lysine pathway is also incomplete, lacking the *dapF* and *lysA* genes, with *dapB* pseudogenized. Moreover, the histidine pathway is disrupted, lacking the two last enzymes of the pathway. In addition, for the methionine pathways, it encodes only the last enzyme. These results suggest potential complementations with the insect, or the secondary endosymbionts, to complete the missing steps (6, 18, 19). Interestingly, "*Ca.* Portiera aleyrodidarum" has the ability to produce carotenoids, compounds that insects usually obtain from the diet. They are a source for insect pigments and have a canonical antioxidant action. Recently, carotenoids have been proposed, using light as a source to generate electrons, to reduce NAD^+ in the pea aphid (17).

The genome of this species from the B biotype has been recently described (15). Gene content in the two genomes is the same, although there are some discrepancies due to differences in annotation (pseudogenes, hypothetical proteins, and noncoding RNA genes). The average nucleotide identity between genes of the two strains is 99.3%.

In summary, we propose "*Ca.* Portiera aleyrodidarum" as a symbiont able not only to supplement the diet of its host but to use carotenoids as a way of protecting against oxidative stresses by supplying it with reducing power.

Nucleotide sequence accession number. The genome was deposited in GenBank under accession number CP003835.

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